

SEQUENCE LISTING

<110> Eijiro WATANABE
Kenji OEDA

<120> Raffinose Synthase Genes and Their Use

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<150> JP 10/120550

<151> 1998-04-30

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<151> 1998-12-04

<150> JP 10/351246

<151> 1998-12-10

<160> 53

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			20					25					30		
Lys	Leu	Leu	Lys	Lys	Leu	Val	Leu	Pro	Asp	Gly	Ser	Ile	Leu	Arg	Cys
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Gln	His	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Cys	Leu	Phe	Val	Asp	Pro	Leu
	50					55					60				
His	Asp	Gly	Lys	Thr	Met	Leu	Lys	Ile	Trp	Asn	Leu	Asn	Lys	Cys	Ser
	65				70					75				80	
Gly	Val	Leu	Gly	Leu	Phe	Asn	Cys	Gln	Gly	Gly	Gly	Trp	Cys	Pro	Val
				85				90						95	
Thr	Arg	Arg	Asn	Lys	Ser	Ser	Ser	Asp	Tyr	Ser	His	Ser	Val	Thr	Cys
			100					105					110		
Phe	Ala	Ser	Pro	Gln	Asp	Ile	Glu	Trp	Gly	Lys	Gly	Lys	His	Pro	Val
		115					120					125			
Cys	Ile	Lys	Gly	Val	Asp	Val	Phe	Ala	Val	Tyr	Met	Phe	Lys	Asp	Asp
	130					135					140				
Lys	Leu	Lys	Leu	Leu	Lys	Tyr	Thr	Glu	Ser	Val	Glu	Val	Ser	Leu	Glu
	145				150					155				160	
Pro	Phe	Ser	Cys	Glu	Leu	Leu	Thr	Val	Ser	Pro	Val	Val	Ile	Leu	Pro
				165				170						175	
Arg	Lys	Ser	Ile	Gln	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn	Met	Leu	Asn
		180					185						190		
Ser	Gly	Gly	Ser	Ile	Met	Ser	Leu	Glu	Phe	Asp	Gln	Gln	Glu	Asn	Leu
		195					200				205				
Ala	Arg	Ile	Gly	Val	Arg	Gly	His	Gly	Glu	Met	Arg	Val	Phe	Ala	Ser
	210					215					220				
Glu	Lys	Pro	Glu	Ser	Val	Lys	Ile	Asp	Gly	Glu	Ser	Val	Glu	Phe	Asp

10525 U.S. PTO

09/30/766



04/29/99

Av 1649
Zaphrent

225 230 235 240
 Tyr Val Asp Arg Thr Val Arg Leu Gln Val Ser Trp Pro Cys Ser Ser
 245 250 255
 Arg Leu Ser Val Val Glu Tyr Leu Phe
 260 265

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 <222> (2)...(799)

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 Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Lys His Asn
 20 25 30
 ttc aag ttg ctt aag aag ctt gtt cta cct gat ggc tcc att ttg cgg 142
 Phe Lys Leu Leu Lys Lys Leu Val Leu Pro Asp Gly Ser Ile Leu Arg
 35 40 45
 tgt caa cat tat gca ctt ccc acc cga gac tgc tta ttt gta gat cct 190
 Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Val Asp Pro
 50 55 60
 tta cat gat ggg aaa aca atg ctc aaa att tgg aac ctc aat aaa tgt 238
 Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu Asn Lys Cys
 65 70 75
 tcc ggg gtt ttg ggt ctg ttc aat tgc caa gga gga ggt tgg tgc cct 286
 Ser Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp Cys Pro
 80 85 90 95
 gtt act agg cga aac aag agt agc tct gac tat tca cac tcc gtg act 334
 Val Thr Arg Arg Asn Lys Ser Ser Ser Asp Tyr Ser His Ser Val Thr
 100 105 110
 tgc ttt gca agt cct caa gac att gaa tgg ggc aaa ggg aag cac cca 382
 Cys Phe Ala Ser Pro Gln Asp Ile Glu Trp Gly Lys Gly Lys His Pro
 115 120 125
 gtt tgc atc aaa ggg gtg gac gta ttt gct gtg tac atg ttt aag gac 430
 Val Cys Ile Lys Gly Val Asp Val Phe Ala Val Tyr Met Phe Lys Asp
 130 135 140
 gac aag ttg aag ctg ctg aag tac aca gag agt gta gaa gtt tct ctt 478
 Asp Lys Leu Lys Leu Leu Lys Tyr Thr Glu Ser Val Glu Val Ser Leu
 145 150 155
 gag cct ttt agt tgt gag ctt ttg acc gtt tct cca gtg gtg atc tta 526
 Glu Pro Phe Ser Cys Glu Leu Leu Thr Val Ser Pro Val Val Ile Leu
 160 165 170 175
 ccc aga aaa tca atc caa ttt gcc cca att gga ttg gta aac atg ctc 574
 Pro Arg Lys Ser Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu
 180 185 190
 aac tct ggg ggc tct att atg tca ttg gaa ttt gat caa cag gaa aat 622
 Asn Ser Gly Gly Ser Ile Met Ser Leu Glu Phe Asp Gln Gln Glu Asn
 195 200 205
 ttg gcg agg att ggg gtg aga gga cat ggg gaa atg agg gta ttt gca 670
 Leu Ala Arg Ile Gly Val Arg Gly His Gly Glu Met Arg Val Phe Ala
 210 215 220
 tca gag aag cca gag agt gtc aag att gat gga gaa tct gtg gaa ttt 718
 Ser Glu Lys Pro Glu Ser Val Lys Ile Asp Gly Glu Ser Val Glu Phe

225	230	235	
gat tat gtt gat aga acc gtg agg ctc caa gtc tcg tgg cct tgt tct			766
Asp Tyr Val Asp Arg Thr Val Arg Leu Gln Val Ser Trp Pro Cys Ser			
240	245	250	255
tcg agg ttg tcc gta gtc gag tat ttg ttc tga atcatgattt ggtgtccgag			819
Ser Arg Leu Ser Val Val Glu Tyr Leu Phe			
260	265		
agagccgtgt aatgttcaca taaactgact taagtgcatt aagcaaatacc accttaaata			879
atagtgcata actttgttcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			928

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 <212> PRT
 <213> Beta vulgaris L.

<400> 3

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Ala	Asn	His	Asp	Cys	Asn	Thr	Cys	Pro	Ile	Ile	Ser	Leu	Glu	Glu	
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Ser	Asn	Phe	Met	Val	Asn	Gly	His	Val	Ile	Leu	Ser	Gln	Val	Pro	Ser
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Asn	Ile	Thr	Ala	Ile	Ser	Lys	Met	Gly	Phe	Asp	Gly	Leu	Phe	Val	Gly
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Phe	Asp	Ala	Pro	Glu	Pro	Lys	Ala	Arg	His	Val	Val	Ser	Val	Gly	Gln
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Leu	Lys	Gly	Ile	Pro	Phe	Met	Ser	Ile	Phe	Arg	Phe	Lys	Val	Trp	Trp
				85					90					95	
Thr	Thr	His	Trp	Thr	Gly	Ser	Asn	Gly	Arg	Asp	Leu	Glu	His	Glu	Thr
			100					105					110		
Gln	Ile	Leu	Ile	Leu	Asp	Lys	Ser	Asp	Glu	Gly	Leu	Gly	Arg	Pro	Tyr
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Ile	Val	Ile	Leu	Pro	Leu	Ile	Glu	Gly	Pro	Phe	Arg	Ala	Ser	Leu	Gln
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Thr	Lys	Val	Val	Gly	Asp	Ser	Phe	Arg	Ala	Val	Leu	Tyr	Ile	Arg	Ala
				165				170						175	
Gly	Pro	Asp	Pro	Phe	Lys	Leu	Ile	Lys	Asp	Thr	Met	Lys	Glu	Val	Gln
		180						185					190		
Ala	His	Leu	Gly	Thr	Phe	Lys	Leu	Leu	Asp	Asp	Lys	Thr	Pro	Pro	Gly
	195						200					205			
Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Lys
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Val	Glu	Pro	Tyr	Gly	Val	Trp	Glu	Gly	Val	Lys	Gly	Leu	Val	Glu	Asn
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Gly	Val	Pro	Pro	Gly	Leu	Val	Leu	Ile	Asp	Asp	Gly	Trp	Gln	Ser	Ile
				245					250					255	
Cys	His	Asp	Asp	Asp	Pro	Ile	Thr	Asp	Gln	Glu	Gly	Ile	Asn	Arg	Thr
		260						265					270		
Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Ile	Lys	Tyr	Glu	Glu	Asn
	275						280					285			
Phe	Lys	Phe	Arg	Asp	Tyr	Lys	Ser	Pro	Asn	Ile	Met	Gly	His	Glu	Asp
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His	Pro	Asn	Met	Gly	Met	Arg	Ala	Phe	Val	Arg	Asp	Leu	Lys	Glu	Glu
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Phe	Lys	Thr	Val	Glu	His	Val	Tyr	Val	Trp	His	Ala	Phe	Thr	Gly	Tyr
				325					330					335	
Trp	Gly	Gly	Val	Arg	Pro	Asn	Val	Pro	Gly	Leu	Pro	Glu	Ala	Gln	Val
			340					345						350	

Val	Thr	Pro	Lys	Leu	Ser	Pro	Gly	Leu	Glu	Met	Thr	Met	Glu	Asp	Leu	355	360	365
Ala	Val	Asp	Lys	Ile	Val	Asn	Asn	Gly	Ile	Gly	Leu	Val	Gln	Pro	Asp	370	375	380
Lys	Ala	Gln	Glu	Leu	Tyr	Glu	Gly	Leu	His	Ser	His	Leu	Glu	Asn	Cys	385	390	395
Gly	Ile	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His	Leu	Leu	Glu	Met	Met	405	410	415
Ala	Glu	Asp	Tyr	Gly	Gly	Arg	Val	Glu	Leu	Ala	Lys	Thr	Tyr	Tyr	Lys	420	425	430
Ala	Ile	Thr	Glu	Ser	Val	Arg	Lys	His	Phe	Lys	Gly	Asn	Gly	Val	Ile	435	440	445
Ala	Ser	Met	Glu	Gln	Cys	Asn	Asp	Phe	Met	Leu	Leu	Gly	Thr	Glu	Thr	450	455	460
Ile	Cys	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Pro	Thr	Asp	Pro	Ser	465	470	475
Gly	Asp	Ile	Asn	Gly	Thr	Tyr	Trp	Leu	Gln	Gly	Cys	His	Met	Val	His	485	490	495
Cys	Ala	Tyr	Asn	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	His	Pro	Asp	Trp	500	505	510
Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	His	Ala	Ala	Ser	515	520	525
Arg	Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser	Asp	Val	Val	Gly	Lys	530	535	540
His	Asn	Ile	Pro	Leu	Leu	Lys	Arg	Leu	Val	Leu	Ala	Asp	Gly	Ser	Ile	545	550	555
Leu	Arg	Cys	Glu	Tyr	His	Ala	Leu	Pro	Thr	Lys	Asp	Cys	Leu	Phe	Val	565	570	575
Asp	Pro	Leu	His	Asp	Gly	Lys	Thr	Met	Leu	Lys	Ile	Trp	Asn	Leu	Asn	580	585	590
Lys	Tyr	Asn	Gly	Val	Leu	Gly	Val	Phe	Asn	Cys	Gln	Gly	Gly	Gly	Trp	595	600	605
Ser	Arg	Glu	Ser	Arg	Lys	Asn	Leu	Cys	Phe	Ser	Glu	Tyr	Ser	Lys	Pro	610	615	620
Ile	Ser	Cys	Lys	Thr	Ser	Pro	Lys	Asp	Val	Glu	Trp	Glu	Asn	Gly	His	625	630	635
Lys	Pro	Phe	Pro	Ile	Lys	Gly	Val	Glu	Cys	Phe	Ala	Met	Tyr	Phe	Thr	645	650	655
Lys	Glu	Lys	Lys	Leu	Ile	Leu	Ser	Gln	Leu	Ser	Asp	Thr	Ile	Glu	Ile	660	665	670
Ser	Leu	Asp	Pro	Phe	Asp	Tyr	Glu	Leu	Ile	Val	Val	Ser	Pro	Met	Thr	675	680	685
Ile	Leu	Pro	Trp	Glu	Ser	Ile	Ala	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn	690	695	700
Met	Leu	Asn	Ala	Gly	Gly	Ala	Val	Lys	Ser	Leu	Asp	Ile	Ser	Glu	Asp	705	710	715
Asn	Glu	Asp	Lys	Met	Val	Gln	Val	Gly	Ile	Lys	Gly	Ala	Gly	Glu	Met	725	730	735
Met	Val	Tyr	Ser	Ser	Glu	Lys	Pro	Lys	Ala	Cys	Arg	Val	Asn	Gly	Glu	740	745	750
Asp	Met	Glu	Phe	Glu	Tyr	Glu	Glu	Ser	Met	Ile	Lys	Val	Gln	Val	Thr	755	760	765
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<211> 2690

<212> DNA

<213> Beta vulgaris L.

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ttgtggggat atttataact atcatattat ttgtgtagat cattctacaa aaaagagagt	180
gagttttttt agctcttatt tcctaagaaa ttaatagcaa aagtttttgca taact atg	238
	Met
gct cca agc ttt agc aag gaa aat tcc aag acg tgt gat gag gtt gca	286
Ala Pro Ser Phe Ser Lys Glu Asn Ser Lys Thr Cys Asp Glu Val Ala	
5 10 15	
aac cat gat gat tgc aac acg tgt cca ata att tcc ttg gaa gaa tca	334
Asn His Asp Asp Cys Asn Thr Cys Pro Ile Ile Ser Leu Glu Glu Ser	
20 25 30	
aac ttc atg gtg aat ggt cac gtg ata ttg tcc caa gtt cca tcc aac	382
Asn Phe Met Val Asn Gly His Val Ile Leu Ser Gln Val Pro Ser Asn	
35 40 45	
atc acg gcc att agt aaa atg ggt ttt gat ggg ctt ttt gtg ggt ttt	430
Ile Thr Ala Ile Ser Lys Met Gly Phe Asp Gly Leu Phe Val Gly Phe	
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gat gct cca gag ccc aag gcc cgg cac gtt gta tcc gtg ggc cag ctc	478
Asp Ala Pro Glu Pro Lys Ala Arg His Val Val Ser Val Gly Gln Leu	
70 75 80	
aag gga att ccc ttc atg agt atc ttc agg ttc aag gta tgg tgg act	526
Lys Gly Ile Pro Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr	
85 90 95	
acc cat tgg act ggg tcc aat ggg cgg gac ctt gag cat gag acc caa	574
Thr His Trp Thr Gly Ser Asn Gly Arg Asp Leu Glu His Glu Thr Gln	
100 105 110	
att ctc atc ctt gat aag tca gat gaa ggt ttg ggc cgt ccc tat att	622
Ile Leu Ile Leu Asp Lys Ser Asp Glu Gly Leu Gly Arg Pro Tyr Ile	
115 120 125	
gtg atc ctc cca ttg atc gaa ggc cca ttt cgg gca tct ctc cag ccg	670
Val Ile Leu Pro Leu Ile Glu Gly Pro Phe Arg Ala Ser Leu Gln Pro	
130 135 140 145	
ggg tct gtt gat gac tat gtg gat ata tgt gtt gag agt ggg tcc act	718
Gly Ser Val Asp Asp Tyr Val Asp Ile Cys Val Glu Ser Gly Ser Thr	
150 155 160	
aaa gtt gtc gga gac tcg ttc cgg gct gtt ctt tat ata cgg gct ggg	766
Lys Val Val Gly Asp Ser Phe Arg Ala Val Leu Tyr Ile Arg Ala Gly	
165 170 175	
cct gac cca ttt aag tta att aaa gat aca atg aag gaa gtc caa gcc	814
Pro Asp Pro Phe Lys Leu Ile Lys Asp Thr Met Lys Glu Val Gln Ala	
180 185 190	
cat tta ggg act ttc aaa ctc tta gat gac aaa act cct cca gga ata	862
His Leu Gly Thr Phe Lys Leu Leu Asp Asp Lys Thr Pro Pro Gly Ile	
195 200 205	
gtg gac aag ttt gga tgg tgt aca tgg gat gca ttt tac ctc aaa gta	910
Val Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr Leu Lys Val	
210 215 220 225	
gag ccw tat ggt gtt tgg gaa gga gtt aaa gga ctc gtc gaa aac ggg	958
Glu Pro Tyr Gly Val Trp Glu Gly Val Lys Gly Leu Val Glu Asn Gly	
230 235 240	
gtc cca ccc ggt ctc gta ctc att gat gat ggg tgg caa tct att tgt	1006
Val Pro Pro Gly Leu Val Leu Ile Asp Asp Gly Trp Gln Ser Ile Cys	
245 250 255	
cat gac gat gat ccg att acc gac caa gaa ggg ata aac cgg act tct	1054
His Asp Asp Asp Pro Ile Thr Asp Gln Glu Gly Ile Asn Arg Thr Ser	
260 265 270	

gcc ggc gag caa atg cca tgt aga ttg atc aag tac gag gaa aac ttc	1102
Ala Gly Glu Gln Met Pro Cys Arg Leu Ile Lys Tyr Glu Glu Asn Phe	
275 280 285	
aag ttt agg gac tat aaa agc cca aat att atg ggc cat gag gat cat	1150
Lys Phe Arg Asp Tyr Lys Ser Pro Asn Ile Met Gly His Glu Asp His	
290 295 300 305	
ccc aat atg gga atg agg gcc ttt gtt agg gac ctt aag gag gag ttc	1198
Pro Asn Met Gly Met Arg Ala Phe Val Arg Asp Leu Lys Glu Glu Phe	
310 315 320	
aaa act gtt gag cat gtg tat gtt tgg cat gct ttt acg ggc tat tgg	1246
Lys Thr Val Glu His Val Tyr Val Trp His Ala Phe Thr Gly Tyr Trp	
325 330 335	
gga ggg gta agg ccc aat gtt cca ggc cta ccr gag gcc caa gta gta	1294
Gly Gly Val Arg Pro Asn Val Pro Gly Leu Pro Glu Ala Gln Val Val	
340 345 350	
acc cca aag ctt tcc ccg ggt ctt gag atg aca atg gaa gat cta gct	1342
Thr Pro Lys Leu Ser Pro Gly Leu Glu Met Thr Met Glu Asp Leu Ala	
355 360 365	
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Val Asp Lys Ile Val Asn Asn Gly Ile Gly Leu Val Gln Pro Asp Lys	
370 375 380 385	
gcc caa gaa ctt tat gaa ggg ttg cat tct cat ttg gaa aat tgt ggg	1438
Ala Gln Glu Leu Tyr Glu Gly Leu His Ser His Leu Glu Asn Cys Gly	
390 395 400	
att gat gga gtc aaa gtt gat gtc atc cat ttg ttg gag atg atg gca	1486
Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Met Met Ala	
405 410 415	
gag gac tat gga gga aga gtt gaa cta gca aaa aca tac tat aag gca	1534
Glu Asp Tyr Gly Gly Arg Val Glu Leu Ala Lys Thr Tyr Tyr Lys Ala	
420 425 430	
ata aca gaa tca gtg cgt aag cat ttc aaa ggc aac ggt gtg att gct	1582
Ile Thr Glu Ser Val Arg Lys His Phe Lys Gly Asn Gly Val Ile Ala	
435 440 445	
agc atg gag cag tgc aac gat ttc atg ctc ctt ggt act gag acc att	1630
Ser Met Glu Gln Cys Asn Asp Phe Met Leu Leu Gly Thr Glu Thr Ile	
450 455 460 465	
tgt ctt ggt cgc gtt ggg gat gac ttt tgg cca act gat ccg tct gga	1678
Cys Leu Gly Arg Val Gly Asp Asp Phe Trp Pro Thr Asp Pro Ser Gly	
470 475 480	
gat ata aat ggt aca tat tgg ctc caa ggc tgt cat atg gtg cat tgt	1726
Asp Ile Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val His Cys	
485 490 495	
gcc tac aat agc tta tgg atg gga aac ttt ata cac cct gac tgg gac	1774
Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile His Pro Asp Trp Asp	
500 505 510	
atg ttc caa tct aca cac cct tgt gct gaa ttt cat gct gca tct cgt	1822
Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala Ser Arg	
515 520 525	
gcg att tct ggt gga cca att tat gtt agt gat gtt gtt ggc aag cat	1870
Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Val Val Gly Lys His	
530 535 540 545	
aac atc ccc ttg ctc aaa agg ctc gtc ttg gct gat ggt tcg atc ctt	1918
Asn Ile Pro Leu Leu Lys Arg Leu Val Leu Ala Asp Gly Ser Ile Leu	
550 555 560	
cgt tgc gag tac cat gca ctt cct act aag gat tgc cta ttt gta gat	1966
Arg Cys Glu Tyr His Ala Leu Pro Thr Lys Asp Cys Leu Phe Val Asp	
565 570 575	
cct ttg cac gat ggc aaa aca atg ctc aaa att tgg aac ctc aac aag	2014
Pro Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu Asn Lys	
580 585 590	
tac aat gga gtg ctt gga gtc ttc aat tgc caa gga gga ggg tgg agc	2062

Tyr	Asn	Gly	Val	Leu	Gly	Val	Phe	Asn	Cys	Gln	Gly	Gly	Gly	Trp	Ser		
595						600					605						
cgt	gag	tct	cga	aaa	aat	cta	tgt	ttc	tca	gag	tat	tca	aaa	cct	att	2110	
Arg	Glu	Ser	Arg	Lys	Asn	Leu	Cys	Phe	Ser	Glu	Tyr	Ser	Lys	Pro	Ile		
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Ser	Cys	Lys	Thr	Ser	Pro	Lys	Asp	Val	Glu	Trp	Glu	Asn	Gly	His	Lys		
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cca	ttc	ccc	atc	aaa	gga	gtg	gaa	tgt	ttt	gcc	atg	tac	ttc	acc	aag	2206	
Pro	Phe	Pro	Ile	Lys	Gly	Val	Glu	Cys	Phe	Ala	Met	Tyr	Phe	Thr	Lys		
				645					650					655			
gaa	aaa	aag	cta	atc	ctc	tca	caa	cta	tct	gac	acc	att	gaa	ata	tca	2254	
Glu	Lys	Lys	Leu	Ile	Leu	Ser	Gln	Leu	Ser	Asp	Thr	Ile	Glu	Ile	Ser		
		660					665					670					
ctt	gat	ccc	ttc	gat	tac	gag	ctt	att	gta	gtc	tct	ccg	atg	aca	att	2302	
Leu	Asp	Pro	Phe	Asp	Tyr	Glu	Leu	Ile	Val	Val	Ser	Pro	Met	Thr	Ile		
		675				680					685						
cta	ccc	tgg	gag	tcg	atc	gca	ttt	gca	ccc	ata	gga	tta	gta	aac	atg	2350	
Leu	Pro	Trp	Glu	Ser	Ile	Ala	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn	Met		
690					695					700					705		
ctc	aac	gcc	gga	ggg	gca	gtc	aag	tct	ttg	gac	atc	agt	gag	gat	aat	2398	
Leu	Asn	Ala	Gly	Gly	Ala	Val	Lys	Ser	Leu	Asp	Ile	Ser	Glu	Asp	Asn		
				710					715					720			
gag	gat	aag	atg	gtt	cag	gtt	ggg	att	aaa	ggg	gcc	gga	gaa	atg	atg	2446	
Glu	Asp	Lys	Met	Val	Gln	Val	Gly	Ile	Lys	Gly	Ala	Gly	Glu	Met	Met		
		725					730						735				
gtt	tat	tca	tca	gaa	aag	cca	aaa	gcg	tgt	aga	gtt	aat	gga	gaa	gac	2494	
Val	Tyr	Ser	Ser	Glu	Lys	Pro	Lys	Ala	Cys	Arg	Val	Asn	Gly	Glu	Asp		
		740					745					750					
atg	gag	ttt	gag	tat	gaa	gag	agc	atg	att	aag	gtt	caa	gtt	aca	tgg	2542	
Met	Glu	Phe	Glu	Tyr	Glu	Glu	Ser	Met	Ile	Lys	Val	Gln	Val	Thr	Trp		
		755				760				765							
aac	cat	aac	tca	ggg	ggg	ttt	acc	act	gtt	gag	tac	tta	ttt	tga	gcttg	2592	
Asn	His	Asn	Ser	Gly	Gly	Phe	Thr	Thr	Val	Glu	Tyr	Leu	Phe				
770					775					780							
aagcta	aatct	aagtc	tttac	ttaat	gagtg	atgta	actga	gtagt	tgact	tgagag	taca					2652	
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<210> 5

<211> 777

<212> PRT

<213> Brassica juncea

<400> 5

Met	Ala	Pro	Pro	Ser	Val	Ile	Lys	Ser	Asp	Ala	Ala	Val	Asn	Gly	Ile		
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Asp	Leu	Ser	Gly	Lys	Pro	Leu	Phe	Arg	Leu	Glu	Gly	Ser	Asp	Leu	Leu		
			20					25					30				
Ala	Asn	Gly	His	Val	Val	Leu	Thr	Asp	Val	Pro	Val	Asn	Val	Thr	Val		
			35				40						45				
Thr	Ala	Ser	Pro	Tyr	Leu	Ala	Asp	Lys	Asp	Gly	Glu	Pro	Val	Asp	Ala		
			50			55					60						
Ser	Ala	Gly	Ser	Phe	Ile	Gly	Phe	Asn	Leu	Asp	Gly	Glu	Pro	Arg	Ser		
			65		70				75					80			
Arg	His	Val	Ala	Ser	Ile	Gly	Lys	Leu	Arg	Asp	Ile	Arg	Phe	Met	Ser		
				85				90						95			
Ile	Phe	Arg	Phe	Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val	Gly	Ser	Lys		
			100				105						110				
Gly	Ser	Asp	Ile	Glu	Asn	Glu	Thr	Gln	Ile	Ile	Ile	Leu	Glu	Asn	Ser		
			115				120						125				

Gly	Ser	Gly	Arg	Pro	Tyr	Val	Leu	Leu	Leu	Pro	Leu	Leu	Glu	Gly	Ser	130	135	140	
Phe	Arg	Ser	Ser	Phe	Gln	Pro	Gly	Glu	Asp	Asp	Val	Ala	Val	Cys	145	150	155	160	
Val	Glu	Ser	Gly	Ser	Thr	Gln	Val	Thr	Gly	Ser	Glu	Phe	Arg	Gln	Val	165	170	175	
Val	Tyr	Val	His	Ala	Gly	Asp	Asp	Pro	Phe	Lys	Leu	Val	Lys	Asp	Ala	180	185	190	
Met	Lys	Val	Val	Arg	Val	His	Met	Asn	Thr	Phe	Lys	Leu	Leu	Glu	Glu	195	200	205	
Lys	Thr	Pro	Pro	Gly	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	210	215	220	
Ala	Phe	Tyr	Leu	Thr	Val	Asn	Pro	Asp	Gly	Val	His	Lys	Gly	Val	Lys	225	230	235	240
Cys	Leu	Val	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Leu	Val	Leu	Ile	Asp	Asp	245	250	255	
Gly	Trp	Gln	Ser	Ile	Gly	His	Asp	Ser	Asp	Gly	Ile	Asp	Val	Glu	Gly	260	265	270	
Met	Ser	Cys	Thr	Val	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Leu	Lys	275	280	285	
Phe	Gln	Glu	Asn	Phe	Lys	Phe	Arg	Asp	Tyr	Val	Ser	Pro	Lys	Asp	Lys	290	295	300	
Asn	Glu	Val	Gly	Met	Lys	Ala	Phe	Val	Arg	Asp	Leu	Lys	Glu	Glu	Phe	305	310	315	320
Ser	Thr	Val	Asp	Tyr	Ile	Tyr	Val	Trp	His	Ala	Leu	Cys	Gly	Tyr	Trp	325	330	335	
Gly	Gly	Leu	Arg	Pro	Gly	Ala	Pro	Thr	Leu	Pro	Pro	Ser	Thr	Ile	Val	340	345	350	
Arg	Pro	Glu	Leu	Ser	Pro	Gly	Leu	Lys	Leu	Thr	Met	Gln	Asp	Leu	Ala	355	360	365	
Val	Asp	Lys	Ile	Val	Asp	Thr	Gly	Ile	Gly	Phe	Val	Ser	Pro	Asp	Met	370	375	380	
Ala	Asn	Glu	Phe	Tyr	Glu	Gly	Leu	His	Ser	His	Leu	Gln	Asn	Val	Gly	385	390	395	400
Ile	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His	Ile	Leu	Glu	Met	Leu	Cys	405	410	415	
Glu	Lys	Tyr	Gly	Gly	Arg	Val	Asp	Leu	Ala	Lys	Ala	Tyr	Phe	Lys	Ala	420	425	430	
Leu	Thr	Ser	Ser	Val	Asn	Lys	His	Phe	Asp	Gly	Asn	Gly	Val	Ile	Ala	435	440	445	
Ser	Met	Glu	His	Cys	Asn	Asp	Phe	Met	Phe	Leu	Gly	Thr	Glu	Ala	Ile	450	455	460	
Ser	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr	Asp	Pro	Ser	Gly	465	470	475	480
Asp	Ile	Asn	Gly	Thr	Tyr	Trp	Leu	Gln	Gly	Cys	His	Met	Val	His	Cys	485	490	495	
Ala	Tyr	Asn	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	Gln	Pro	Asp	Trp	Asp	500	505	510	
Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	His	Ala	Ala	Ser	Arg	515	520	525	
Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Ile	Ser	Asp	Cys	Val	Gly	Gln	His	530	535	540	
Asp	Phe	Asp	Leu	Leu	Lys	Arg	Leu	Val	Leu	Pro	Asp	Gly	Ser	Ile	Leu	545	550	555	560
Arg	Cys	Glu	His	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Arg	Leu	Phe	Glu	Asp	565	570	575	
Pro	Leu	His	Asp	Gly	Lys	Thr	Met	Leu	Lys	Ile	Trp	Asn	Leu	Asn	Lys	580	585	590	
Tyr	Thr	Gly	Ile	Ile	Gly	Ala	Phe	Asn	Cys	Gln	Gly	Gly	Gly	Trp	Cys	595	600	605	
Arg	Glu	Thr	Arg	Arg	Asn	Gln	Cys	Phe	Ser	Gln	Cys	Val	Asn	Thr	Leu				

610	615	620
Thr Ala Thr Thr Asn Pro Lys Asp Val Glu Trp Asn Ser Gly Asn Asn		
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Pro Ile Ser Val Glu Asn Val Glu Glu Phe Ala Leu Phe Leu Ser Gln		640
	645	650
Ser Lys Lys Leu Val Leu Ser Gly Pro Asn Asp Asp Leu Glu Ile Thr		655
	660	665
Leu Glu Pro Phe Lys Phe Glu Leu Ile Thr Val Ser Pro Val Val Thr		670
	675	680
Ile Glu Gly Ser Ser Val Gln Phe Ala Pro Ile Gly Leu Val Asn Met		685
	690	695
Leu Asn Thr Ser Gly Ala Ile Arg Ser Leu Val Tyr His Glu Glu Ser		700
705	710	715
Val Glu Ile Gly Val Arg Gly Ala Gly Glu Phe Arg Val Tyr Ala Ser		720
	725	730
Arg Lys Pro Ala Ser Cys Lys Ile Asp Gly Glu Val Val Glu Phe Gly		735
	740	745
Tyr Glu Glu Ser Met Val Met Val Gln Val Pro Trp Ser Ala Pro Glu		750
	755	760
Gly Leu Ser Ser Ile Lys Tyr Glu Phe		765
770	775	777

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 <212> DNA
 <213> Brassica juncea

<220>
 <221> CDS
 <222> (134)...(2467)

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tctatcagcg aaa atg gct cca ccg agc gta att aaa tcc gat gct gca	169
Met Ala Pro Pro Ser Val Ile Lys Ser Asp Ala Ala	
5 10	
gtc aac ggc att gac ctc tcc gga aag ccg ctt ttc cgg cta gag ggt	217
Val Asn Gly Ile Asp Leu Ser Gly Lys Pro Leu Phe Arg Leu Glu Gly	
15 20 25	
tcc gat ctc cta gcc aat ggt cac gtt gtc tta acc gat gta ccg gtt	265
Ser Asp Leu Leu Ala Asn Gly His Val Val Leu Thr Asp Val Pro Val	
30 35 40	
aac gtg act gtc act gct tca cct tac cta gct gac aaa gac gga gaa	313
Asn Val Thr Val Thr Ala Ser Pro Tyr Leu Ala Asp Lys Asp Gly Glu	
45 50 55 60	
ccg gtt gac gcc tcc gct ggt tca ttc atc ggg ttt aat ctc gac ggt	361
Pro Val Asp Ala Ser Ala Gly Ser Phe Ile Gly Phe Asn Leu Asp Gly	
65 70 75	
gag cca cga agc cgc cac gtg gcg tcc atc ggt aaa ctc agg gat att	409
Glu Pro Arg Ser Arg His Val Ala Ser Ile Gly Lys Leu Arg Asp Ile	
80 85 90	
cga ttc atg agc ata ttc cgt ttc aag gtt tgg tgg act act cac tgg	457
Arg Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp	
95 100 105	
gtc ggt tcc aaa gga tcc gac atc gag aac gag acc cag atc atc atc	505
Val Gly Ser Lys Gly Ser Asp Ile Glu Asn Glu Thr Gln Ile Ile Ile	
110 115 120	
ctc gag aac tcc ggg tcg ggt cgt cct tat gtt ctt ctt ctg ccg ctt	553
Leu Glu Asn Ser Gly Ser Gly Arg Pro Tyr Val Leu Leu Leu Pro Leu	

125	130	135	140	
ctt gaa ggc tct ttc	cgt tca tcc ttt cag cct ggg gaa gac gat gac			601
Leu Glu Gly Ser Phe	Arg Ser Ser Phe Gln Pro Gly Glu Asp Asp Asp			
	145	150	155	
gtg gcg gtt tgt gtc	gaa tcc ggg tcg acc cag gtg acc ggg tcg gag			649
Val Ala Val Cys Val	Glu Ser Gly Ser Thr Gln Val Thr Gly Ser Glu			
	160	165	170	
ttt cgt caa gtt gtg	tat gtt cac gcc gga gac gat ccg ttc aag ctc			697
Phe Arg Gln Val Val	Tyr Val His Ala Gly Asp Asp Pro Phe Lys Leu			
	175	180	185	
gtg aaa gac gcg atg	aag gtg gtt agg gtt cat atg aac acc ttc aag			745
Val Lys Asp Ala Met	Lys Val Arg Val His Met Asn Thr Phe Lys			
	190	195	200	
ctc ttg gaa gag aag	acr ccg ccg gga atc gtc gat aag ttc ggg tgg			793
Leu Leu Glu Glu Lys	Thr Pro Pro Gly Ile Val Asp Lys Phe Gly Trp			
	205	210	215	
tgc acg tgg gat gcg	ttt tat ttg acg gtg aac cct gac gga gtt cat			841
Cys Thr Trp Asp Ala	Phe Tyr Leu Thr Val Asn Pro Asp Gly Val His			
	225	230	235	
aag ggt gtt aag tgt	ctc gtc gac ggt ggt tgt ccg ccg gga ttg gtc			889
Lys Gly Val Lys Cys	Leu Val Asp Gly Gly Cys Pro Pro Gly Leu Val			
	240	245	250	
cta atc gac gac ggt	tgg caa tcg att gga cat gac tcc gat ggt atc			937
Leu Ile Asp Asp Gly	Trp Gln Ser Ile Gly His Asp Ser Asp Gly Ile			
	255	260	265	
gat gtt gaa ggg atg	agt tgt acc gtc gcc ggg gag caa atg cct tgc			985
Asp Val Glu Gly Met	Ser Cys Thr Val Ala Gly Glu Gln Met Pro Cys			
	270	275	280	
agg ctt ctg aaa ttt	caa gag aac ttc aag ttc aga gac tac gtc tct			1033
Arg Leu Leu Lys Phe	Gln Glu Asn Phe Lys Phe Arg Asp Tyr Val Ser			
	285	290	295	
ccg aaa gac aaa aac	gaa gtc ggg atg aaa gct ttc gtc aga gat ctg			1081
Pro Lys Asp Lys Asn	Glu Val Gly Met Lys Ala Phe Val Arg Asp Leu			
	305	310	315	
aaa gaa gaa ttc tcc	acc gtt gat tac atc tac gtc tgg cac gcg ctt			1129
Lys Glu Glu Phe Ser	Thr Val Asp Tyr Ile Tyr Val Trp His Ala Leu			
	320	325	330	
tgc ggc tac tgg ggt	ggt ctt cgt ccc gga gct cct act ctt ccg ccc			1177
Cys Gly Tyr Trp Gly	Gly Leu Arg Pro Gly Ala Pro Thr Leu Pro Pro			
	335	340	345	
tca act att gtc cgg	cca gag ctc tcg ccg ggg ctt aag ttg acg atg			1225
Ser Thr Ile Val Arg	Pro Glu Leu Ser Pro Gly Leu Lys Leu Thr Met			
	350	355	360	
caa gat ctc gcc gtt	gat aag att gtc gat acc gga atc gga ttc gtc			1273
Gln Asp Leu Ala Val	Asp Lys Ile Val Asp Thr Gly Ile Gly Phe Val			
	365	370	375	
tcg ccg gac atg gcg	aat gag ttt tac gaa ggt ctt cac tct cat ctt			1321
Ser Pro Asp Met Ala	Asn Glu Phe Tyr Glu Gly Leu His Ser His Leu			
	385	390	395	
caa aac gtc ggt att	gac ggc gtt aaa gtt gac gtc atc cac ata ttg			1369
Gln Asn Val Gly Ile	Asp Gly Val Lys Val Asp Val Ile His Ile Leu			
	400	405	410	
gag atg ttg tgc gag	aaa tat ggc ggg aga gta gac ttg gct aaa gct			1417
Glu Met Leu Cys Glu	Lys Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala			
	415	420	425	
tac ttc aag gcg tta	act tcc tca gtg aat aag cat ttt gac ggt aac			1465
Tyr Phe Lys Ala Leu	Thr Ser Val Asn Lys His Phe Asp Gly Asn			
	430	435	440	
ggc gtt atc gct agc	atg gag cac tgt aat gat ttc atg ttc ctt gga			1513
Gly Val Ile Ala Ser	Met Glu His Cys Asn Asp Phe Met Phe Leu Gly			
	445	450	455	
				460

acc gaa gcc atc tct cta ggt cgt gtc ggt gat gac ttt tgg tgc acg	1561
Thr Glu Ala Ile Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr	
465 470 475	
gat cca tca ggc gac ata aac ggc aca tat tgg ctg caa gga tgc cac	1609
Asp Pro Ser Gly Asp Ile Asn Gly Thr Tyr Trp Leu Gln Gly Cys His	
480 485 490	
atg gtc cac tgt gcc tac aac agt ctt tgg atg gga aat ttc atc cag	1657
Met Val His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln	
495 500 505	
cct gat tgg gac atg ttt cag tcc aca cat cct tgt gct gag ttc cat	1705
Pro Asp Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His	
510 515 520	
gct gct tct cgt gcc atc tcc ggt ggg ccc att tac atc agc gat tgt	1753
Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Ile Ser Asp Cys	
525 530 535 540	
gtg ggc cag cac gat ttc gat ctc ttg aag cga ctc gtc ttg cct gac	1801
Val Gly Gln His Asp Phe Asp Leu Leu Lys Arg Leu Val Leu Pro Asp	
545 550 555	
ggg tgc att ttg agg tgt gag cac tat gca ctc cca act cgt gac cgt	1849
Gly Ser Ile Leu Arg Cys Glu His Tyr Ala Leu Pro Thr Arg Asp Arg	
560 565 570	
ctc ttt gaa gac cct ctt cat gat ggc aaa acc atg ctc aag att tgg	1897
Leu Phe Glu Asp Pro Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp	
575 580 585	
aac ttg aac aag tac act gga att att gga gca ttc aac tgc caa gga	1945
Asn Leu Asn Lys Tyr Thr Gly Ile Ile Gly Ala Phe Asn Cys Gln Gly	
590 595 600	
gga gga tgg tgc aga gaa acc cga cgc aac caa tgc ttc tcc caa tgc	1993
Gly Gly Trp Cys Arg Glu Thr Arg Arg Asn Gln Cys Phe Ser Gln Cys	
605 610 615 620	
gtt aac acg tta acc gcc aca aca aat cct aag gac gtt gaa tgg aac	2041
Val Asn Thr Leu Thr Ala Thr Thr Asn Pro Lys Asp Val Glu Trp Asn	
625 630 635	
agt ggg aac aac cca atc tcc gtt gaa aac gtt gaa gag ttt gct ttg	2089
Ser Gly Asn Asn Pro Ile Ser Val Glu Asn Val Glu Glu Phe Ala Leu	
640 645 650	
ttc ttg tct cag tct aag aag ctt gtg ttg tct gga cca aac gat gat	2137
Phe Leu Ser Gln Ser Lys Lys Leu Val Leu Ser Gly Pro Asn Asp Asp	
655 660 665	
ctc gag atc act ttg gag cct ttc aag ttt gag cta atc act gtc tca	2185
Leu Glu Ile Thr Leu Glu Pro Phe Lys Phe Glu Leu Ile Thr Val Ser	
670 675 680	
cca gtt gtc act att gag ggt agt tcg gtt cag ttt gct cca atc gga	2233
Pro Val Val Thr Ile Glu Gly Ser Ser Val Gln Phe Ala Pro Ile Gly	
685 690 695 700	
ttg gtt aac atg cta aac act agc ggt gca att cga tcc ttg gtg tat	2281
Leu Val Asn Met Leu Asn Thr Ser Gly Ala Ile Arg Ser Leu Val Tyr	
705 710 715	
cat gag gaa tcc gtt gag att gga gtt cgt ggt gct gga gag ttc agg	2329
His Glu Glu Ser Val Glu Ile Gly Val Arg Gly Ala Gly Glu Phe Arg	
720 725 730	
gtt tat gca tca agg aaa cct gcg agc tgc aaa att gat ggt gaa gtt	2377
Val Tyr Ala Ser Arg Lys Pro Ala Ser Cys Lys Ile Asp Gly Glu Val	
735 740 745	
gtt gag ttt gga tac gaa gag tca atg gtg atg gtt caa gtg cct tgg	2425
Val Glu Phe Gly Tyr Glu Glu Ser Met Val Met Val Gln Val Pro Trp	
750 755 760	
tct gca ccc gag ggt ttg tct tct att aag tat gag ttt tag agtttccga	2476
Ser Ala Pro Glu Gly Leu Ser Ser Ile Lys Tyr Glu Phe	
765 770 775	
aggtgcttat ttgtatcctt ctaaactcct taattatgag ctccgtgccg tttctttttc	2536

Gly	Trp	Cys	Arg	Glu	Thr	Arg	Arg	Asp	Gln	Cys	Phe	Ser	Gln	Cys	Val	
				405					410					415		
Asn	Thr	Leu	Thr	Ala	Thr	Thr	Asn	Pro	Asn	Asp	Val	Glu	Trp	Asn	Ser	
				420				425					430			
Gly	Asn	Asn	Pro	Ile	Ser	Ile	Glu	Asn	Val	Glu	Glu	Phe	Ala	Leu	Phe	
		435					440					445				
Leu	Ser	Gln	Ser	Lys	Lys	Leu	Val	Leu	Ser	Gly	Gln	Asn	Asp	Asp	Leu	
	450					455					460					
Glu	Ile	Thr	Leu	Glu	Pro	Phe	Lys	Phe	Glu	Leu	Ile	Thr	Val	Ser	Pro	
465					470				475						480	
Val	Val	Thr	Ile	Glu	Gly	Ser	Ser	Val	Gln	Phe	Ala	Pro	Ile	Gly	Leu	
				485					490					495		
Val	Asn	Met	Leu	Asn	Thr	Ser	Gly	Ala	Ile	Arg	Ser	Leu	Val	Tyr	His	
			500					505					510			
Glu	Glu	Ser	Val	Glu	Ile	Gly	Val	Arg	Gly	Ala	Gly	Glu	Phe	Arg	Val	
		515					520					525				
Tyr	Ala	Ser	Lys	Lys	Pro	Val	Ser	Cys	Lys	Ile	Asp	Gly	Glu	Asp	Val	
	530					535					540					
Glu	Phe	Gly	Tyr	Glu	Glu	Ser	Met	Val	Met	Val	Gln	Val	Pro	Trp	Ser	
545					550				555						560	
Ala	Pro	Glu	Gly	Leu	Ser	Ser	Ile	Lys	Tyr	Leu	Phe					
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 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)...(1719)

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Leu	Glu	Glu	Lys	Thr	Pro	Pro	Gly	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	
				5					10					15		
acg	tgg	gat	gcg	ttt	tat	ttg	acg	gtg	aac	cct	gac	gga	gtt	cat	aag	96
Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Thr	Val	Asn	Pro	Asp	Gly	Val	His	Lys	
			20				25					30				
ggg	gtt	aag	tgt	ctc	gtc	gac	ggg	ggg	tgt	ccg	ccg	gga	ttg	gtc	cta	144
Gly	Val	Lys	Cys	Leu	Val	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Leu	Val	Leu	
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atc	gac	gac	ggg	tgg	caa	tgc	att	gga	cat	gac	tcc	gat	ggg	atc	gat	192
Ile	Asp	Asp	Gly	Trp	Gln	Ser	Ile	Gly	His	Asp	Ser	Asp	Gly	Ile	Asp	
	50					55				60						
gtt	gaa	ggg	atg	agt	tgt	acc	gtc	gcc	ggg	gag	caa	atg	cct	tgc	agg	240
Val	Glu	Gly	Met	Ser	Cys	Thr	Val	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	
	65				70				75					80		
ctt	ccg	aaa	ttt	caa	gag	aac	ttc	aag	ttc	aga	gac	tac	gtc	tct	ccg	288
Leu	Pro	Lys	Phe	Gln	Glu	Asn	Phe	Lys	Phe	Arg	Asp	Tyr	Val	Ser	Pro	
				85					90					95		
aaa	gac	aaa	aac	gaa	gtc	ggg	atg	aaa	gct	ttc	gtc	aga	gat	ctg	aaa	336
Lys	Asp	Lys	Asn	Glu	Val	Gly	Met	Lys	Ala	Phe	Val	Arg	Asp	Leu	Lys	
			100					105					110			
gaa	gaa	ttc	tcc	acc	gtt	gat	tac	atc	tac	gtc	tgg	cac	gcg	ctt	tgc	384
Glu	Glu	Phe	Ser	Thr	Val	Asp	Tyr	Ile	Tyr	Val	Trp	His	Ala	Leu	Cys	
		115					120					125				
ggg	tac	tgg	ggw	ggg	ctt	cgt	ccc	gga	gct	cct	act	ctt	ccg	ccs	tcr	432
Gly	Tyr	Trp	Gly	Gly	Leu	Arg	Pro	Gly	Ala	Pro	Thr	Leu	Pro	Pro	Ser	
	130					135					140					

act	att	gtc	cgr	cca	gag	ctc	tcg	ccg	ggg	ctt	aag	ttg	acg	atg	caa	480
Thr	Ile	Val	Arg	Pro	Glu	Leu	Ser	Pro	Gly	Leu	Lys	Leu	Thr	Met	Gln	
145					150					155					160	
gat	ctc	gcc	gtt	gat	aag	atc	atc	gat	acc	gga	atc	gga	ttc	gtc	tcg	528
Asp	Leu	Ala	Val	Asp	Lys	Ile	Ile	Asp	Thr	Gly	Ile	Gly	Phe	Val	Ser	
				165					170					175		
ccg	gac	atg	gcg	aac	gag	ttt	tac	gaa	ggg	ctt	cac	tct	cat	ctt	caa	576
Pro	Asp	Met	Ala	Asn	Glu	Phe	Tyr	Glu	Gly	Leu	His	Ser	His	Leu	Gln	
			180					185					190			
aac	gtc	ggc	att	aac	ggc	gtt	aaa	gtt	gac	gtt	atc	cac	ata	ctg	gag	624
Asn	Val	Gly	Ile	Asn	Gly	Val	Lys	Val	Asp	Val	Ile	His	Ile	Leu	Glu	
	195					200						205				
atg	ttg	tgc	gag	aaa	tat	ggc	ggg	aga	gtt	gac	ttg	gct	aaa	gct	tac	672
Met	Leu	Cys	Glu	Lys	Tyr	Gly	Gly	Arg	Val	Asp	Leu	Ala	Lys	Ala	Tyr	
	210					215				220						
ttc	aag	gcg	tta	acg	tcg	tca	gtg	aat	aag	cat	ttt	gac	ggc	aac	gcc	720
Phe	Lys	Ala	Leu	Thr	Ser	Ser	Val	Asn	Lys	His	Phe	Asp	Gly	Asn	Ala	
225					230					235				240		
gtt	atc	gcc	agc	atg	gag	cac	tgt	aat	gac	ttc	atg	ttc	ctt	gga	acc	768
Val	Ile	Ala	Ser	Met	Glu	His	Cys	Asn	Asp	Phe	Met	Phe	Leu	Gly	Thr	
				245					250					255		
gaa	gcc	atc	tct	cta	ggg	cgt	gtc	ggg	gat	gac	ttt	tgg	tgc	acg	gat	816
Glu	Ala	Ile	Ser	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr	Asp	
			260					265					270			
cca	tct	ggc	gac	att	aac	ggc	acg	tat	tgg	ctg	caa	gga	tgt	cac	atg	864
Pro	Ser	Gly	Asp	Ile	Asn	Gly	Thr	Tyr	Trp	Leu	Gln	Gly	Cys	His	Met	
		275				280						285				
gtc	cac	tgt	gcc	tac	aac	agt	ctt	tgg	atg	gga	aat	ttc	atc	cag	cct	912
Val	His	Cys	Ala	Tyr	Asn	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	Gln	Pro	
	290				295					300						
gat	tgg	gac	atg	ttt	cag	tcc	aca	cat	cct	tgt	gct	gag	ttc	cat	gct	960
Asp	Trp	Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	His	Ala	
305				310					315						320	
gct	tca	cgt	gcc	atc	tcc	ggg	ggg	ccc	att	tac	atc	agc	gat	tgt	gtg	1008
Ala	Ser	Arg	Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Ile	Ser	Asp	Cys	Val	
				325				330						335		
ggc	cag	cac	gat	ttc	gat	ctc	ttg	agg	aga	ctc	gtt	ttg	cct	gac	ggg	1056
Gly	Gln	His	Asp	Phe	Asp	Leu	Leu	Arg	Arg	Leu	Val	Leu	Pro	Asp	Gly	
			340					345				350				
tcg	att	ttg	agg	tgt	gag	tac	tat	gct	ctc	cca	act	cgt	gac	cgt	ctc	1104
Ser	Ile	Leu	Arg	Cys	Glu	Tyr	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Arg	Leu	
		355					360					365				
ttt	gaa	gac	cct	ctt	cat	gat	ggc	aaa	acc	atg	ctc	aag	att	tgg	aac	1152
Phe	Glu	Asp	Pro	Leu	His	Asp	Gly	Lys	Thr	Met	Leu	Lys	Ile	Trp	Asn	
	370					375				380						
ttg	aac	aag	tac	act	gga	atc	atc	gga	gca	ttc	aac	tgt	caa	gga	gga	1200
Leu	Asn	Lys	Tyr	Thr	Gly	Ile	Ile	Gly	Ala	Phe	Asn	Cys	Gln	Gly	Gly	
385					390				395					400		
gga	tgg	tgc	aga	gaa	act	cga	cgc	gac	caa	tgc	ttc	tcc	caa	tgc	gtt	1248
Gly	Trp	Cys	Arg	Glu	Thr	Arg	Arg	Asp	Gln	Cys	Phe	Ser	Gln	Cys	Val	
				405				410						415		
aac	acg	tta	acc	gcc	aca	aca	aat	cct	aat	gac	gtt	gaa	tgg	aac	agt	1296
Asn	Thr	Leu	Thr	Ala	Thr	Thr	Asn	Pro	Asn	Asp	Val	Glu	Trp	Asn	Ser	
			420					425					430			
ggg	aac	aac	ccg	atc	tcc	att	gaa	aac	gtt	gaa	gag	ttt	gct	ttg	ttc	1344
Gly	Asn	Asn	Pro	Ile	Ser	Ile	Glu	Asn	Val	Glu	Glu	Phe	Ala	Leu	Phe	
		435					440					445				
ttg	tct	caa	tcc	aag	aag	ctt	gtg	ttg	tcc	ggg	caa	aac	gat	gat	ctc	1392
Leu	Ser	Gln	Ser	Lys	Lys	Leu	Val	Leu	Ser	Gly	Gln	Asn	Asp	Asp	Leu	
	450					455				460						
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[illegible]

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<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

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<211> 30
<212> DNA
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<220>
<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

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ggaacaaagt tatgcactat tattttaaggt 30
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<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence
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<220>
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<400> 11
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<210> 12
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 <213> Artificial Sequence

 <220>
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 <400> 12
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 <210> 13
 <211> 30
 <212> DNA
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 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

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 <210> 14
 <211> 30
 <212> DNA
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 <220>
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 <210> 15
 <211> 30
 <212> DNA
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 <210> 16
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
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<400> 16
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<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 17
accaatccaa aatctcatca aataatcgca 30

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 18
aaataatagg ggcagtacaa attacaccac 30

<210> 19
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 19
atggctccac cgagcgtaat taaatccga 29

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 20
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<210> 21
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene, n is i.

<400> 21
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<210> 22
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene, n is i, r is a or g.

<400> 22
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<210> 23
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene.

<400> 23
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<210> 24
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene, n is i.

<400> 24
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<210> 25
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene, n is i, y is t or c, r is a or g.

<400> 25
 atytttrtcna cngcnarrtc ytccatngt 29

<210> 26
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene, n is i, y is t or c.

 <400> 26
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 <210> 27
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene, n is i, r is a or g.

 <400> 27
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 <210> 28
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene.

 <400> 28
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 <210> 29
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase
 gene.

 <400> 29
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 <210> 30
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
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 gene.

<400> 30

aagcatgccca aacatacaca tgctcaacag

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<210> 31

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 31

agaccgggg aaagctttgg ggttactact

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<210> 32

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 32

tggatgggaa actttataca ccctgact

28

<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 33

gacatgttcc catctacaca cccttggtg

28

<210> 34

<211> 30

<212> DNA

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<220>

<223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 34

ccaatttatg ttagtgatgt tgttggcaag

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<210> 35

<211> 26

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<213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 35
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<210> 36
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene, n is i.

<400> 36
 cgattnaang tntggtggac nacncantgg gtngg
 35

<210> 37
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene, n is i, r is a or g.

<400> 37
 cantgnacca tntgncancc ntgnarccan tangtncc
 38

<210> 38
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 38
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<210> 39
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 39
 caacggcgag atcttgcac gtcaac
 26

<210> 40
 <211> 30
 <212> DNA
 <213> Artificial Sequence

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 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

 <400> 40
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 <210> 41
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

 <400> 41
 ccacgtgcac caccggaact tatcgac 27

 <210> 42
 <211> 30
 <212> DNA
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 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

 <400> 42
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 <210> 43
 <211> 30
 <212> DNA
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 <220>
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 <400> 43
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 <210> 44
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 44
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<210> 45
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 45
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<210> 46
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 46
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<210> 47
 <211> 35
 <212> DNA
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<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 47
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<210> 48
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to obtain raffinose synthase gene.

<400> 48
 acaatagttg agggcggaag agtag 25

<210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide linker to obtain raffinose synthase gene.

 <400> 49
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 <210> 50
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide linker to obtain raffinose synthase gene.

 <400> 50
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 <210> 51
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to confirm direction of the inserted raffinose synthase gene.

 <400> 51
 cctcctcgga ttccattgcc cagctatctg 30

 <210> 52
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to confirm direction of the inserted raffinose synthase gene.

 <400> 52
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 <210> 53
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to confirm direction of the inserted raffinose synthase gene.

 <400> 53
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